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## RAW SEQUENCE LISTING

DATE: 12/04/2001

PATENT APPLICATION: US/09/978,486

TIME: 19:48:31

Input Set : N:\Crf3\RULE60\09978486.raw

Output Set: N:\CRF3\12042001\I978486.raw

ENTERED

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1 <110> APPLICANT: Lin, Yi-Jyun
2      Benzer, Seymour
3      California Institute of Technology
4 <120> TITLE OF INVENTION: METHUSELAH GENE, COMPOSITIONS AND
5      METHODS OF USE
6 <130> FILE REFERENCE: 06618/343001
7 <140> CURRENT APPLICATION NUMBER: 09/978,486
8 <141> CURRENT FILING DATE: 2001-10-15
9 <150> PRIOR APPLICATION NUMBER: US/09/370,098
10 <151> PRIOR FILING DATE: 1999-08-06
11 <150> PRIOR APPLICATION NUMBER: 60/095,826
12 <151> PRIOR FILING DATE: 1998-08-07
13 <160> NUMBER OF SEQ ID NOS: 6
14 <170> SOFTWARE: FastSEQ for Windows Version 4.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 1972
18 <212> TYPE: DNA
19 <213> ORGANISM: Drosophila Melanogaster
20 <220> FEATURE:
21 <221> NAME/KEY: CDS
22 <222> LOCATION: (130)...(1679)
23 <400> SEQUENCE: 1
24      taaagtttag ttgtcacaca catctgtgtg agttttaagc ttaaaaaaag ttcaaacgcg      60
25      gaacgtccat gtccgcttga tacagaacgt ccatgtccgc ttgatacacc gatcgagaac      120
26      aaaaaagca taa atg aaa act ctt ttg gtt ctt cgg ata tca act gtc ata      171
27      * Met Lys Thr Leu Leu Val Leu Arg Ile Ser Thr Val Ile
28      1          5          10
29      ctt gtt gtg ctg gtt att caa aaa tca tat gca gac att ctc gaa tgc      219
30      Leu Val Val Leu Val Ile Gln Lys Ser Tyr Ala Asp Ile Leu Glu Cys
31      15          20          25
32      gat tat ttc gac act gtc gat att tcg gca gct caa aaa cta cag aat      267
33      Asp Tyr Phe Asp Thr Val Asp Ile Ser Ala Ala Gln Lys Leu Gln Asn
34      30          35          40          45
35      gga tcg tac tta ttt gag ggg ttg ctc gtt ccg gcc att ttg acg gga      315
36      Gly Ser Tyr Leu Phe Glu Gly Leu Leu Val Pro Ala Ile Leu Thr Gly
37      50          55          60
38      gaa tat gac ttt agg att ctc ccg gac gac tcg aag cag aag gtg gct      363
39      Glu Tyr Asp Phe Arg Ile Leu Pro Asp Asp Ser Lys Gln Lys Val Ala
40      65          70          75
41      cgt cac ata aga gga tgt gtg tgc aag ctg aag ccc tgt gtc aga ttt      411
42      Arg His Ile Arg Gly Cys Val Cys Lys Leu Lys Pro Cys Val Arg Phe
43      80          85          90
44      Met Ser Asp Glu Glu Leu Ala Glu Leu Asp Pro Phe Leu Asn Val Thr

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49	110	115	120	125	
50	ctt gac gac ggg tcg gtg tcc cgc aga cac ttt aaa aac gaa cta atc	555			
51	Leu Asp Asp Gly Ser Val Ser Arg Arg His Phe Lys Asn Glu Leu Ile				
52	130 135 140				
53	gtc cag tgg gac cta ccg atg ccg tgt gac gga atg ttc tac cta gac	603			
54	Val Gln Trp Asp Leu Pro Met Pro Cys Asp Gly Met Phe Tyr Leu Asp				
55	145 150 155				
56	aac cgc gaa gaa cag gat aag tac acg ttg ttc gag aac gga act ttc	651			
57	Asn Arg Glu Glu Gln Asp Lys Tyr Thr Leu Phe Glu Asn Gly Thr Phe				
58	160 165 170				
59	ttt cgc cac ttt gac cgt gtg act ctt cgc aag cgg gaa tac tgc ctt	699			
60	Phe Arg His Phe Asp Arg Val Thr Leu Arg Lys Arg Glu Tyr Cys Leu				
61	175 180 185				
62	cag cat ctt aca ttc gca gat ggt aat gct acg tct att cga att gca	747			
63	Gln His Leu Thr Phe Ala Asp Gly Asn Ala Thr Ser Ile Arg Ile Ala				
64	190 195 200 205				
65	cct cac aac tgt ttg ata gtg cca tca att acc ggt cag acg gtt gtg	795			
66	Pro His Asn Cys Leu Ile Val Pro Ser Ile Thr Gly Gln Thr Val Val				
67	210 215 220				
68	atg atc tct tcg ctg ata tgc atg gtt cta acg atc gcc gta tac ctc	843			
69	Met Ile Ser Ser Leu Ile Cys Met Val Leu Thr Ile Ala Val Tyr Leu				
70	225 230 235				
71	ttc gtc aag aaa cta caa aac ttg cat gga aaa tgc ttc atc tgc tac	891			
72	Phe Val Lys Lys Leu Gln Asn Leu His Gly Lys Cys Phe Ile Cys Tyr				
73	240 245 250				
74	atg gtg tgt ctc ttt atg gga tat ctt ttc cta ttg ctc gat ttg tgg	939			
75	Met Val Cys Leu Phe Met Gly Tyr Leu Phe Leu Leu Leu Asp Leu Trp				
76	255 260 265				
77	cag ata tcc att agc ttt tgc aaa cca gca ggt ttt ctg ggt tac ttc	987			
78	Gln Ile Ser Ile Ser Phe Cys Lys Pro Ala Gly Phe Leu Gly Tyr Phe				
79	270 275 280 285				
80	ttt gtc atg gcc gca ttt ttt tgg ctt tcc gtc atc agt ctg cac ctt	1035			
81	Phe Val Met Ala Ala Phe Phe Trp Leu Ser Val Ile Ser Leu His Leu				
82	290 295 300				
83	tgg aac acg ttc aga ggc tcc tcc cac aaa gcg aat cgc ttc tta ttt	1083			
84	Trp Asn Thr Phe Arg Gly Ser Ser His Lys Ala Asn Arg Phe Leu Phe				
85	305 310 315				
86	gag cat cgg ttt ctg gcc tac aat acc tat gct tgg ggc atg gcg gtg	1131			
87	Glu His Arg Phe Leu Ala Tyr Asn Thr Tyr Ala Trp Gly Met Ala Val				
88	320 325 330				
89	gtc ctg aca gga att acc gtt ctg gcc gat aac atc gtg gaa aac cag	1179			
90	Val Leu Thr Gly Ile Thr Val Leu Ala Asp Asn Ile Val Glu Asn Gln				
91	335 340 345				
92	gat tgg aat cct cgt gtg ggc cac gag gga cac tgt tgg ata tat act	1227			
93	Asp Trp Asn Pro Arg Val Gly His Glu Gly His Cys Trp Ile Tyr Thr				
94	350 355 360 365				
95	gag ggc tgg tcc ggc atg gtc tgc ttt tgc ggt gga atg gta ttt gta				

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98      att gcc ttt aac ata acc atg ttc atc ctg acg gct aag cgt ata tta      1323
99      Ile Ala Phe Asn Ile Thr Met Phe Ile Leu Thr Ala Lys Arg Ile Leu
100             385                      390                      395
101      gga gtg aag aag gac att cag aac ttt gcg cac agg caa gag aga aag      1371
102      Gly Val Lys Lys Asp Ile Gln Asn Phe Ala His Arg Gln Glu Arg Lys
103             400                      405                      410
104      cag aag ctg aac tcc gac aaa cag act tac acc ttc ttc cta cgg ctc      1419
105      Gln Lys Leu Asn Ser Asp Lys Gln Thr Tyr Thr Phe Phe Leu Arg Leu
106             415                      420                      425
107      ttc atc att atg gga ttg tcc tgg agc ttg gag ata ggc tcc tac ttt      1467
108      Phe Ile Ile Met Gly Leu Ser Trp Ser Leu Glu Ile Gly Ser Tyr Phe
109             430                      435                      440                      445
110      tcg caa tcc aac caa act tgg gcc aac gtc ttt ctg gtg gct gac tat      1515
111      Ser Gln Ser Asn Gln Thr Trp Ala Asn Val Phe Leu Val Ala Asp Tyr
112             450                      455                      460
113      tta aat tgg tct caa gga atc atc ata ttt ata ctg ttc gtt ctg aag      1563
114      Leu Asn Trp Ser Gln Gly Ile Ile Ile Phe Ile Leu Phe Val Leu Lys
115             465                      470                      475
116      cgc agc acg tgg aga ctc ttg cag gag agc att agg ggg gag ggt gag      1611
117      Arg Ser Thr Trp Arg Leu Leu Gln Glu Ser Ile Arg Gly Glu Gly Glu
118             480                      485                      490
119      gag gta aac aac agt gag gaa gag att tcg cta gaa aac acg acg aca      1659
120      Glu Val Asn Asn Ser Glu Glu Glu Ile Ser Leu Glu Asn Thr Thr Thr
121             495                      500                      505
122      cga aat gtc cta tta tag ga accatcctaa atccacgagg agtgtcattt      1709
123      Arg Asn Val Leu Leu *
124      510
125      ctaacagatc tatggcaagt cgtattaccg tgggaacaac tcctaaaaat aaagcacgga      1769
126      actcgccatt ggcttaaaag ctgtaataag tatatgtttg tatcttatta atattcaaac      1829
127      cataaataac ggtttctgta tatcactttt cttaaaacta ttcaactaac tcagatggat      1889
128      ttaacaccgt ttattgaaca taagatgttt tttaacattt gaaataaaaa ataatactgc      1949
129      aataaaaaaaaa aaaaaaaaaaa aaa      1972
131 <210> SEQ ID NO: 2
132 <211> LENGTH: 514
133 <212> TYPE: PRT
134 <213> ORGANISM: Drosophila Melanogaster
135 <400> SEQUENCE: 2
136      Met Lys Thr Leu Leu Val Leu Arg Ile Ser Thr Val Ile Leu Val Val
137             1                      5                      10                      15
138      Leu Val Ile Gln Lys Ser Tyr Ala Asp Ile Leu Glu Cys Asp Tyr Phe
139             20                      25                      30
140      Asp Thr Val Asp Ile Ser Ala Ala Gln Lys Leu Gln Asn Gly Ser Tyr
141             35                      40                      45
142      Leu Phe Glu Gly Leu Leu Val Pro Ala Ile Leu Thr Gly Glu Tyr Asp
143             50                      55                      60
144      Phe Arg Ile Leu Pro Asp Asp Ser Lys Gln Lys Val Ala Arg His Ile
145             65                      70                      75                      80

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148 His Asp His Ile Met Asp Asn Gly Val Cys Tyr Asp Asn Met Ser Asp
149           100           105           110
150 Glu Glu Leu Ala Glu Leu Asp Pro Phe Leu Asn Val Thr Leu Asp Asp
151           115           120           125
152 Gly Ser Val Ser Arg Arg His Phe Lys Asn Glu Leu Ile Val Gln Trp
153           130           135           140
154 Asp Leu Pro Met Pro Cys Asp Gly Met Phe Tyr Leu Asp Asn Arg Glu
155           145           150           155           160
156 Glu Gln Asp Lys Tyr Thr Leu Phe Glu Asn Gly Thr Phe Phe Arg His
157           165           170           175
158 Phe Asp Arg Val Thr Leu Arg Lys Arg Glu Tyr Cys Leu Gln His Leu
159           180           185           190
160 Thr Phe Ala Asp Gly Asn Ala Thr Ser Ile Arg Ile Ala Pro His Asn
161           195           200           205
162 Cys Leu Ile Val Pro Ser Ile Thr Gly Gln Thr Val Val Met Ile Ser
163           210           215           220
164 Ser Leu Ile Cys Met Val Leu Thr Ile Ala Val Tyr Leu Phe Val Lys
165           225           230           235           240
166 Lys Leu Gln Asn Leu His Gly Lys Cys Phe Ile Cys Tyr Met Val Cys
167           245           250           255
168 Leu Phe Met Gly Tyr Leu Phe Leu Leu Asp Leu Trp Gln Ile Ser
169           260           265           270
170 Ile Ser Phe Cys Lys Pro Ala Gly Phe Leu Gly Tyr Phe Phe Val Met
171           275           280           285
172 Ala Ala Phe Phe Trp Leu Ser Val Ile Ser Leu His Leu Trp Asn Thr
173           290           295           300
174 Phe Arg Gly Ser Ser His Lys Ala Asn Arg Phe Leu Phe Glu His Arg
175           305           310           315           320
176 Phe Leu Ala Tyr Asn Thr Tyr Ala Trp Gly Met Ala Val Val Leu Thr
177           325           330           335
178 Gly Ile Thr Val Leu Ala Asp Asn Ile Val Glu Asn Gln Asp Trp Asn
179           340           345           350
180 Pro Arg Val Gly His Glu Gly His Cys Trp Ile Tyr Thr Gln Ala Trp
181           355           360           365
182 Ser Ala Met Leu Tyr Phe Tyr Gly Pro Met Val Phe Leu Ile Ala Phe
183           370           375           380
184 Asn Ile Thr Met Phe Ile Leu Thr Ala Lys Arg Ile Leu Gly Val Lys
185           385           390           395           400
186 Lys Asp Ile Gln Asn Phe Ala His Arg Gln Glu Arg Lys Gln Lys Leu
187           405           410           415
188 Asn Ser Asp Lys Gln Thr Tyr Thr Phe Phe Leu Arg Leu Phe Ile Ile
189           420           425           430
190 Met Gly Leu Ser Trp Ser Leu Glu Ile Gly Ser Tyr Phe Ser Gln Ser
191           435           440           445
192 Asn Gln Thr Trp Ala Asn Val Phe Leu Val Ala Asp Tyr Leu Asn Trp
193           450           455           460
194 Ser Gln Gly Ile Ile Ile Phe Ile Leu Phe Val Leu Leu Thr Ser Thr

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197          485          490          495
198      Asn Ser Glu Glu Glu Ile Ser Leu Glu Asn Thr Thr Thr Arg Asn Val
199          500          505          510
200      Leu Leu
202 <210> SEQ ID NO: 3
203 <211> LENGTH: 269
204 <212> TYPE: PRT
205 <213> ORGANISM: Drosophila Melanogaster
206 <400> SEQUENCE: 3
207      Asn Cys Leu Ile Val Pro Ser Ile Thr Gly Gln Thr Val Val Met Ile
208          1          5          10          15
209      Ser Ser Leu Ile Cys Met Val Leu Thr Ile Ala Val Tyr Leu Phe Val
210          20          25          30
211      Lys Lys Leu Gln Asn Leu His Gly Lys Cys Phe Ile Cys Tyr Met Val
212          35          40          45
213      Cys Leu Phe Met Gly Tyr Leu Phe Leu Leu Leu Asp Leu Trp Gln Ile
214          50          55          60
215      Ser Ile Ser Phe Cys Lys Pro Ala Gly Phe Leu Gly Tyr Phe Phe Val
216          65          70          75          80
217      Met Ala Ala Phe Phe Trp Leu Ser Val Ile Ser Leu His Leu Trp Asn
218          85          90          95
219      Thr Phe Arg Gly Ser Ser His Lys Ala Asn Arg Phe Leu Phe Glu His
220          100          105          110
221      Arg Phe Leu Ala Tyr Asn Thr Tyr Ala Trp Gly Met Ala Val Val Leu
222          115          120          125
223      Thr Gly Ile Thr Val Leu Ala Asp Asn Ile Val Glu Asn Gln Asp Trp
224          130          135          140
225      Asn Pro Arg Val Gly His Glu Gly His Cys Trp Ile Tyr Thr Gln Ala
226          145          150          155          160
227      Trp Ser Ala Met Leu Tyr Phe Tyr Gly Pro Met Val Phe Leu Ile Ala
228          165          170          175
229      Phe Asn Ile Thr Met Phe Ile Leu Thr Ala Lys Arg Ile Leu Gly Val
230          180          185          190
231      Lys Lys Asp Ile Gln Asn Phe Ala His Arg Gln Glu Arg Lys Gln Lys
232          195          200          205
233      Leu Asn Ser Asp Lys Gln Thr Tyr Thr Phe Phe Leu Arg Leu Phe Ile
234          210          215          220
235      Ile Met Gly Leu Ser Trp Ser Leu Glu Ile Gly Ser Tyr Phe Ser Gln
236          225          230          235          240
237      Ser Asn Gln Thr Trp Ala Asn Val Phe Leu Val Ala Asp Tyr Leu Asn
238          245          250          255
239      Trp Ser Gln Gly Ile Ile Ile Phe Ile Leu Phe Val Leu
240          260          265
242 <210> SEQ ID NO: 4
243 <211> LENGTH: 231
244 <212> TYPE: PRT
245 <213> ORGANISM: Homosapiens

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**VERIFICATION SUMMARY**

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